(carbapenem-resistant), and *Clostridium difficile* (spore). Each test (tape and bacteria combination) was done in 3 or 6 replicates; each bacterial enumeration was the average of duplicate plates. The detection limit for this method is 8 CFU per sample, which is equivalent to 0.9 log10. **Results:** The results for all tapes tested showed a statistically significant lower mean log10 recovery of each of the microorganisms tested for packaged versus unpackaged tape (Figure 1). The mean differences of log10 recoveries from a packaged and unpackaged tape ranged from 2.51 log10 (for *S. aureus* on Micropore S) to 4.64 log10 (for *K. pneumoniae* on Medipore H). This is equivalent to 99%–99.99% cross-contamination protection from the 4 organisms tested. **Conclusions:** Individual packaging of medical tape rolls protects them from external contaminants. Even if the packaging becomes contaminated, the tape retrieved from the package will be significantly less contaminated than it would have been from exposure to the same contaminants without packaging.

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Nursing-Home Patient Functional and Microbiota Status Drive Environmental Contamination with Vancomycin-Resistant Enterococci

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Background: Patient colonization and shedding of vancomycin-resistant enterococci (VRE) is a major source of environmental contamination leading to VRE transmission in nursing homes. We hypothesize that we can inform mitigation strategies by identifying patient clinical and microbiota features associated with environmental contamination with VRE. **Methods:** During a 6-month period of active surveillance in 6 Michigan nursing homes, 245 patients (with 806 follow-up visits) were enrolled. Patient clinical data and swabs for VRE were collected from multiple body sites and high-touch environmental surfaces. In total, 316 perirectal swabs were collected from 137 patients for gut microbiota analysis and community status type (CST) assignment based on taxonomic composition. The associations between VRE colonization pattern, gut microbial CST, and patient factors were examined using multivariable generalized estimating equations, adjusting for patient-and facility-level clustering. We used VRE colonization patterns to group study visits: "uncolonized" (patient−/environment−); "environment-only" (patient−/environment+); "patient-only" (patient+/environment−); "both" (patient+/environment+). **Results:** Across all study visits, VRE colonization on patient hand and groin/perirectal area was positively correlated with VRE contamination of high-touch environmental surfaces, suggesting direct transfer of VRE between patient and environment via patient hands (Figure 1A). We next set out to identify patient factors associated with patient colonization and environmental contamination. At baseline, while patients in the "both" group had anticipated risk factors such as longer prior hospitalization and more frequent broad-spectrum antibiotic use, they were unexpectedly younger than "uncolonized" patients and had similar functional status. This last feature contrasted with the "patient-only" group, characterized by higher urinary catheter use and higher functional dependence, suggestive of lower functional dependence facilitating patient contamination of their environment. No clinical features distinguished "uncolonized" and "environment-only" patients (Table 1). Lastly, in multivariable analyses, we determined the contribution of patient functional status and gut microbiota features to environmental contamination. Low-diversity CST, characterized by reduced anaerobic taxa, was weakly associated with "patient-only" and significantly associated with "both." Notably, high functional dependence was significantly associated with "environment-only" and "patient-only" but not "both," indicating high-functioning patients with disrupted gut microbiota as drivers of environmental contamination (Figure 1B). **Conclusions:** Our findings suggest that antimicrobial exposure disrupts patient gut microbiota, a significant mediator of colonization dynamics between patients and their environment, and that high-functioning patients may be more likely to spread VRE between their body sites and high-touch environmental surfaces (Figure 2). These findings highlight both antibiotic stewardship and patient hand hygiene as important targets for interrupting transmission mediated by environmental contamination.

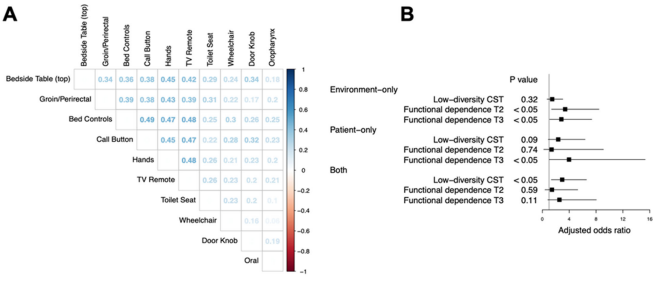

Figure 1 A) Hand and groin colonization with vancomycin-resistant enterococci (VRE) colonization are positively correlated with contamination of high-touch environmental surfaces (Cohen's Kappa statistic). A coefficient of 1 indicates positive correlation and -1 indicates negative correlation. A coefficient less than 0.2 suggests slight agreement; if 0.2–0.4, "fair agreement", if 0.4–0.6, "moderate agreement". **B)** Odds ratio of VRE colonization pattern by functional and gut microbiota status, adjusted for facility and patient-level clustering, and risk factors significantly associated with colonization pattern in univariate analysis (P < .05). Functional dependence was measured by physical self-maintenance score, ranging from 6 (full independence) to 30 (full dependence) in 6 categories of self-maintenance (bathing, dressing, feeding, ambulation, grooming, and toileting), log10 transformed and discretized into tertiles. T1 corresponds to the lowest tertile and lowest dependence, and T3 corresponds to the highest tertile and highest dependence. *0.1, **0.05, ***0.01.

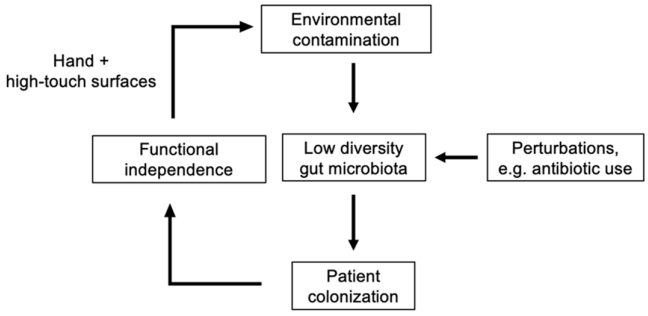

Figure 2. Conceptual model depicting the spread of VRE between environmental and patient sites. Upon exposure to VRE in the environment, patients with high-diversity microbiota are able to resist VRE colonization. However, those with low-diversity microbiota due to perturbations such as antibiotic use are susceptible to VRE colonization in the gut. While low-functioning patients are less likely to interact with their immediate environment, high-functioning patients interact with high-touch surfaces and further propagate environmental contamination.

	No VRE colonization (N = 163)	Environmental (N = 32)	Patient (N = 13)	Both (N = 36)
Age (mean, SD)	73.4 (14)	72 (12.2)	73.2 (14.8)	68 (11.9)**
Male sex (%)	69 (42.3)	17 (53.1)	5 (38.5)	19 (52.8)
Charlson score (mean, SD)	0.5 (0.3)	0.5 (0.3)	0.5 (0.2)	0.5 (0.2)
Urinary catheter (%)	32 (20.4)	8 (25.8)	6 (50)**	6 (17.6)
Hospital stay (SD)	0.8 (0.3)	0.9 (0.3)	0.9 (0.3)	1 (0.2)***
Exposure to narrow-spectrum antibiotic within past 30 days (%)	28 (23.7)	6 (31.6)	2 (28.6)	4 (33.3)
Exposure to broad-spectrum antibiotic within past 30 days (%)	45 (33.3)	13 (50)	6 (54.5)	24 (75)***
Functional dependence T1 (%)	54 (33.1)	8 (25)	1 (7.7)*	9 (25)
Functional dependence T2 (%)	52 (31.9)	11 (34.4)	4 (30.8)	16 (44.4)
Functional dependence T3 (%)	54 (33.1)	13 (40.6)	8 (61.5)*	11 (30.6)

Table 1: Patient characteristics at enrollment and unadjusted univariate analysis, stratified by VRE colonization status. VRE, vancomycin-resistant enterococci. SD, standard deviation. Charlson comorbidity score and length of hospital stay were log transformed. Functional dependence was measured by physical self-maintenance score, ranging from 6 (full independence) to 30 (full dependence) in 6 categories of self-maintenance (bathing, dressing, feeding, ambulation, grooming, and toileting), log10 transformed and discretized into tertiles. T1 corresponds to the lowest tertile and lowest dependence, and T3 corresponds to the highest tertile and highest dependence. *0.1, **0.05, ***0.01.

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